

# CODON USAGE IN PLANTS FREQUENCY TABLE

07/390561

AmAcid	Codon	Number	/1000	Fraction	AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	160.00	10.23	0.12	Tyr	TAT	122.00	7.80	0.24
Gly	GGA	323.00	20.66	0.25	Tyr	TAC	377.00	24.11	0.76
Gly	GGT	355.00	22.70	0.28					
Gly	GGC	445.00	28.46	0.35	Phe	TTT	192.00	12.28	0.28
					Phe	TTC	493.00	31.53	0.72
Glu	GAG	668.00	42.72	0.71					
Glu	GAA	278.00	17.78	0.29	Ser	AGT	97.00	6.20	0.09
					Ser	AGC	280.00	17.91	0.26
Asp	GAT	340.00	21.74	0.45	Ser	TCG	111.00	7.10	0.10
Asp	GAC	422.00	26.99	0.55	Ser	TCA	147.00	9.40	0.14
					Ser	TCT	179.00	11.45	0.17
Val	GTG	390.00	24.94	0.33	Ser	TCC	250.00	15.99	0.23
Val	GTA	69.00	4.41	0.06					
Val	GTT	369.00	23.60	0.32	Arg	AGG	174.00	11.13	0.24
Val	GTC	340.00	21.74	0.29	Arg	AGA	119.00	7.61	0.17
					Arg	CGG	57.00	3.65	0.08
Ala	GCG	214.00	13.69	0.16	Arg	CGA	35.00	2.24	0.05
Ala	GCA	213.00	13.62	0.15	Arg	CGT	145.00	9.27	0.20
Ala	GCT	460.00	29.42	0.33	Arg	CGC	189.00	12.09	0.26
Ala	GCC	490.00	31.34	0.36					
					Gln	CAG	325.00	20.78	0.64
Lys	AAG	726.00	46.43	0.81	Gln	CAA	186.00	11.89	0.36
Lys	AAA	168.00	10.74	0.19					
					His	CAT	151.00	9.66	0.43
Asn	AAT	203.00	12.98	0.32	His	CAC	197.00	12.60	0.57
Asn	AAC	430.00	27.50	0.68					
					Leu	TTG	232.00	14.84	0.18
Met	ATG	376.00	24.05	1.00	Leu	TTA	36.00	2.30	0.03
					Leu	CTG	306.00	19.57	0.24
Ile	ATA	69.00	4.41	0.08	Leu	CTA	65.00	4.16	0.05
Ile	ATT	320.00	20.46	0.39	Leu	CTT	279.00	17.84	0.22
Ile	ATC	434.00	27.75	0.53	Leu	CTC	364.00	23.28	0.28
Thr	ACG	104.00	6.65	0.13	Pro	CCG	222.00	14.20	0.24
Thr	ACA	119.00	7.61	0.15	Pro	CCA	264.00	16.88	0.29
Thr	ACT	232.00	14.84	0.29	Pro	CCT	229.00	14.64	0.25
Thr	ACC	336.00	21.49	0.42	Pro	CCC	200.00	12.79	0.22
Trp	TGG	232.00	14.84	1.00	End	TAG	11.00	0.70	0.23
					End	TAA	21.00	1.34	0.44
Cys	TGT	81.00	5.18	0.29	End	TGA	16.00	1.02	0.33
Cys	TGC	200.00	12.79	0.71					

FIG. 1

SEQUENCE COMPARISON - SYNTHETIC TO NATIVE

This is a comparison of the BT4 synthetic sequence (top line in pair) with the BTS sequence (original sequence of HD-1-Dipel subsp. Kurstaki gene; bottom line in pair). The amino acid sequence is shown above the paired DNA sequences, and is unchanged. Between the pairs, vertical bars are drawn when nucleotides are conserved in the synthetic sequence.

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MetAspAsnAsnProAsnIleAsnGluCysIleProTyrAsnCysLeuSerAsnProG
480 CCATGGACAACAACCCAAACATCAACGAGTGCATCCCATACAACCTCAGCAACCCAG 539
      ||||| ||||| || ||||| || ||||| || || || || || ||||| |
      CCATGGATAACAATCCGAACATCAATGAATGCATTCCCTTATAATTGTTTAAGTAACCCCTG

luValGluValLeuGlyGlyGluArgIleGluThrGlyTyrThrProIleAspIleSerL
540 AGGTGGAGGTGCTCGGCCGCGAGAGGATCGAGACCGGTACACCCCAATCGACATCAGCC 599
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      AAGTAGAAGTATTAGGTGGAGAAAGAATAGAACTGGTTACACCCCAATCGATATTTCTCT

euSerLeuThrGlnPheLeuLeuSerGluPheValProGlyAlaGlyPheValLeuGlyL
600 TCAGCCTCACCCAGTTCCTCCTCAGCGAGTTCGTGCCAGGCGCGGCTTCGTTCCTCGGCC 659
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      TGTCGCTAACGCAATTTCTTTTGTAGTGAATTTGTTCCCGGTGCTGGATTGTGTAGGAC

euValAspIleIleTrpGlyIlePheGlyProSerGlnTrpAspAlaPheProValGlnI
660 TCGTGACATCATCTGGGGCATCTTCGGCCCCAAGCCAGTGGGACGCCTTCCAGTGCAGA 719
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      TAGTTGATATAATATGGGGAATTTTGGTCCCTCTCAATGGGACGCATTTCTGTACAAA

leGluGlnLeuIleAsnGlnArgIleGluGluPheAlaArgAsnGlnAlaIleSerArgL
720 TCGAGCAGCTCATCAACCAGAGGATCGAGGAGTTCGCCAGGAACCAAGGCCATCTCTAGAC 779
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      TTGAACAGTTAATTAACCAAAGAATAGAAGAATTTCGCTAGGAACCAAGCCATTTCTAGAT

euGluGlyLeuSerAsnLeuTyrGlnIleTyrAlaGluSerPheArgGluTrpGluAlaA
780 TTGAGGGCCTCAGCAACCTCTACCAGATCTACGCCGAGAGCTTCAGGGAGTGGGAGGCCG 839
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      TAGAAGGACTAAGCAATCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAG

spProThrAsnProAlaLeuArgGluGluMetArgIleGlnPheAsnAspMetAsnSerA
840 ACCCAACCAACCCAGCCCTCAGGGAGGAGATGCGCATCCAGTTCAACGACATGAACAGTG 899
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      ATCCTACTAATCCAGCATTAAAGAGAAGAGATGCGTATTCAATTCAATGACATGAACAGTG

la
900 CCCT 903
      |||
      CCCT

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FIG. 2

# REACTION WITH KB72 AND KB73 TO DERIVE AMYB12 FROM AMYB15

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KB72  
5' ACAACCATGAGACAACCAACATCAAGAGTGCATCCCATACACTGCCTCAGCAACCCAGAGTGAAGTGC/  
3' - - - - - /

KB73  
5' ACAACCATGAGACAACCAACATCAAGAGTGCATCCCATACACTGCCTCAGCAACCCAGAGTGAAGTGC/  
3' - - - - - /

KB72(continued)  
/TCGCGCGCGAGAGATCGAGACCGGCTAC - - - - - 3'  
/- - - - - CTCTCCTAGCTCTGGCGGATGTGGGTTAGCTGTAGTCGAGTGGGTCAAGAGAGTGGCTCAAGCAGCGGTCCGCGCGGAGACGAGCTGATCAGGC 5'  
KB73(continued)

1. ANNEAL OLIGONUCLEOTIDES KB72 and KB73
2. EXTEND WITH KLENOW POLYMERASE PLUS 4 DEOXYNUCLEOTIDE TRIPHOSPHATES

5' ACAACCATGAGACAACCAACATCAAGAGTGCATCCCATACACTGCCTCAGCAACCCAGAGTGAAGTGC/  
3' TGTGGTACCTGTTGGGTGTGAGTGTCTACGATAGGATATGTTGACGAGTGGTGTGGGTCTCCACCTCCAGC/  
Nco I

5'(con't)  
3'(con't)  
/TCGCGCGCGAGAGATCGAGACCGGCTACACCCCAATGACATCAGCTCAGCCTCACCCAGATTCTCTCCTCAGCGAGTTGTCGCGAGCGCGCGCTTGTGCTCGGACTAGTCCG 3'  
/AGCGCGCGCTCTCTAGCTCTGGCGGATGTGGGTTAGCTGTAGTCGAGTGGGTCAAGAGAGTGGCTCAAGCAGCGGTCCGCGCGGAGCAGAGCTGATCAAGGC 5'  
Spe I

3. PHENOL EXTRACT TO INACTIVATE KLENOW
4. DIGEST WITH NcoI AND SpeI TO REVEAL STICKY ENDS

5' CATGACAACAACCAACATCAAGAGTGCATCCCATACACTGCCTCAGCAACCCAGAGTGAAGTGC/  
3' CTGTGTGGGTGTGAGTGTCTACGATAGGATATGTTGACGAGTGGTGTGGGTCTCCACCTCCAGC/  
Nco I

5'(con't)  
3'(con't)  
/TCGCGCGCGAGAGATCGAGACCGGCTACACCCCAATGACATCAGCTCAGCCTCACCCAGTTCTCTCCTCAGCGAGTTGTCGCAAGCGCGCGGCTTGTGCTCGGA 3'  
/AGCGCGCGCTCTCTAGCTCTGGCGGATGTGGGTTAGCTGTAGTCGAGTGGGTCAAGAGAGTGGCTCAAGCAGCGGTCCGCGCGGAGCAGAGCTGATC 5'  
Spe I

FIG. 3

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REACTION WITH KB74 AND KB75 TO DERIVE AMVBT3 FROM AMVBT2

KB74  
3' CAAGCGCCGCTTCGTTCTCGGCCCTCGTGACATCATCTGGGCATCTTCGCCCAAGCCAG/  
KB75  
3' - - - - -

KB74(continued)  
/TGGAGCGCCTTCCCACTGAGA - - - - - 3'  
/ - TCGGGAAGGCTACGCTAGCTTCGAGTAGTGGTCTCTAGCTCCTCAAGCGGTCTTGGTCCGTAGAGATCTCC 5'  
KB75(continued)

1. ANNEAL OLIGONUCLEOTIDES KB74 and KB75
2. EXTEND WITH KLENOW POLYMERASE AND 4 DEOXYNUCLEOTIDES TRIPHOSPHATES

5' CAAGCGCCGCTTCGTTCTCGGCCCTCGTGACATCATCTGGGCATCTTCGCCCAAGCCAG/  
3' GTTCGCGCCCAAGCAAGACCGGAGCACCTGTAGTAGACCCCGTAGAGCGGGTTGGTC/  
Ban I  
5'(con't) /TGGAGCGCCTTCCCACTGAGATCGACAGCTCATCAACAGAGATCGAGAGTTGCCAAGAACCGCATCTGAGAG 3'  
3'(con't) /ACCTTCGGAAGGCTACGCTAGCTTCGAGTAGTGGTCTCTAGCTCCTCAAGCGGTCTTGGTCCGTAGAGATCTCC 5'  
Xba I

3. PHENOL EXTRACT TO INACTIVATE KLENOW
4. DIGEST WITH Ban I AND Xba I

5' GCGCGGCTTCGTTCTCGGCCCTCGTGACATCATCTGGGCATCTTCGCCCAAGCCAG/  
3' GCGAAGCAAGACCGGAGCACCTGTAGTAGACCCCGTAGAGCGGGTTGGTC/  
Ban I  
5'(con't) /TGGAGCGCCTTCCCACTGAGATCGACAGCTCATCAACAGAGATCGAGAGTTGCCAAGAACCGCATCT 3'  
3'(con't) /ACCTTCGGAAGGCTACGCTAGCTTCGAGTAGTGGTCTCTAGCTCCTCAAGCGGTCTTGGTCCGTAGAGATC 5'  
Xba I

FIG. 4

## REACTION WITH KB76 AND KB77 TO DERIVE AMVB14 FROM AMVB13

KB76

5' CGTCTAGACTTGAGGGCCTCAGCAACCTCTACAGATCTACGCCGAGAGCTT/

KB77

KB76(continued)

/CAGGAGTGGAGGCCGACCCAAAC - - - - - 3'

/ - CTCACCCCTCCGGCTGGTTGCTCAACCTCCGGCTGGTTGGTTAGTACCTCTACGGCTAGTCAAGTTGCTGTACTTGTCAACGGGTC 5'

KB77(continued)

1. ANNEAL OLIGONUCLEOTIDES KB76 and KB77
2. EXTEND WITH KLENOW POLYMERASE AND 4 DEOXYNUCLEOTIDES TRIPHOSPHATES

5' CGTCTAGACTTGAGGGCCTCAGCAACCTCTACAGATCTACGCCGAGAGCTT/  
3' GAGATCTGAACTCCCGAGTCGTTGGAGATGGTTAGATGGGCTCTCGAA/

Xba I

5'(con't) /CAGGAGTGGAGGCCGACCCAAACGAGTGGAGGCCGACCCAAACCAACCCAGCCCTCAGGAGAGATGCCATCCAGTTCAACGACATGAACAGTCCCCAG 3'  
3'(con't) /GTCCCTCAACCCCTCCGGCTGGTTGCTCAACCTCCGGCTGGTTGGTTGGTCCGGAGTCCCTCTACGGCTAGGTCAAGTTGCTGTACTTGTCACGGGTC 5'

Bsp 1286

3. PHENOL EXTRACT TO INACTIVATE KLENOW
4. DIGEST WITH Xba I AND Bsp 1286

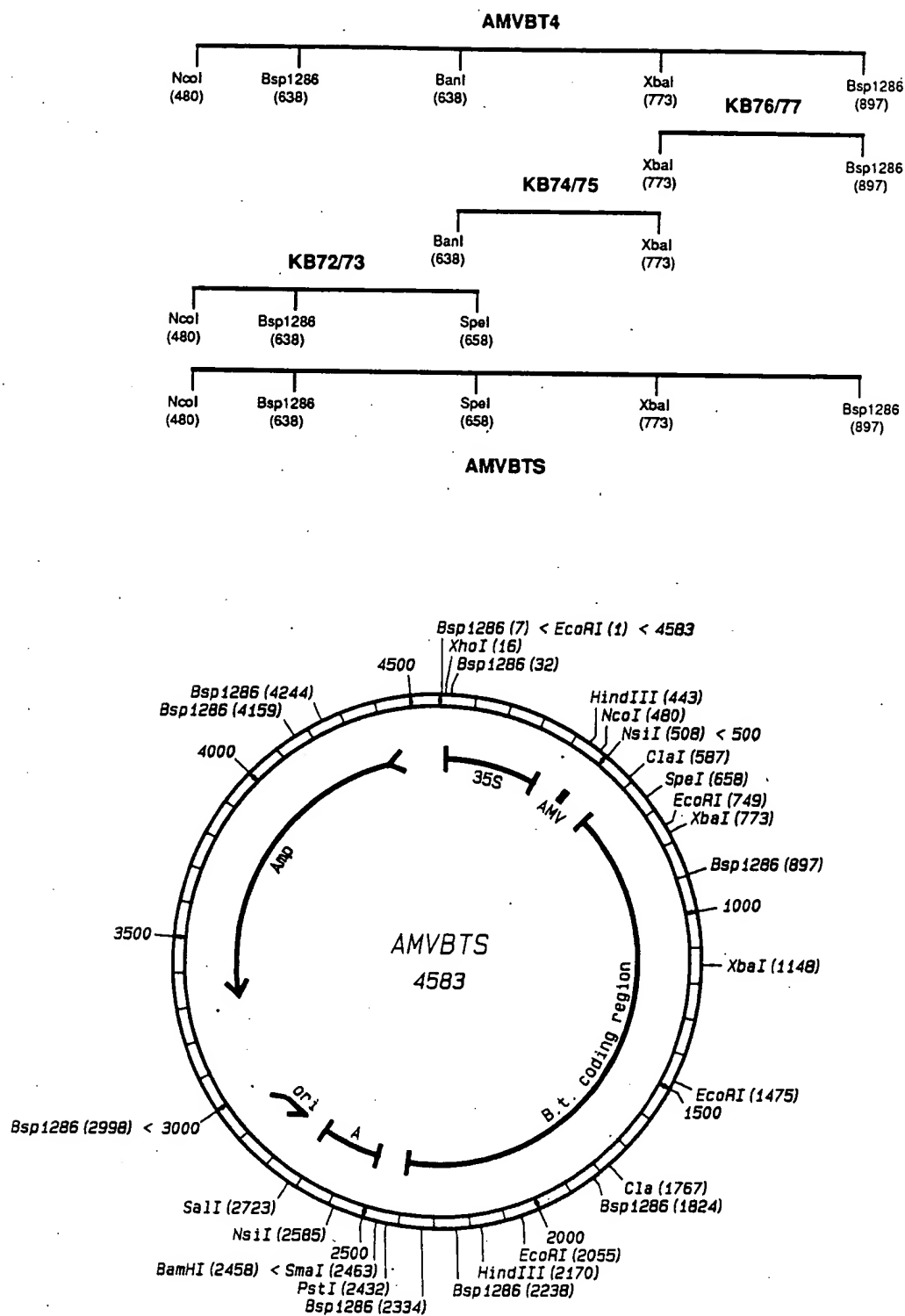
5' CTAGACTTGAGGGCCTCAGCAACCTCTACAGATCTACGCCGAGAGCTT/  
3' TGAACCTCCCGAGTCGTTGGAGATGGTTAGATGGGCTCTCGAA/  
Xba I

5'(con't) /CAGGAGTGGAGGCCGACCCAAACGAGTGGAGGCCGACCCAAACCAACCCAGCCCTCAGGAGAGATGCCATCCAGTTCAACGACATGAACAGTCCCC 3'  
3'(con't) /GTCCCTCAACCCCTCCGGCTGGTTGCTCAACCTCCGGCTGGTTGGTTGGTCCGGAGTCCCTCTACGGCTAGGTCAAGTTGCTGTACTTGTC 5'

Bsp 1286

FIG. 5

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**FIG. 6**